Amendments to the Specification:

Please replace the paragraph beginning at page 11, line 31 as with the following amended paragraph:

~~Figure 1~~Figures 1A and 1B ~~depicts~~ depict a proposed biosynthetic pathway for BL. CR goes through at least two different pathways, referred to as the early C-6 oxidation (right column) and late C-6 oxidation (left column) pathways. Steps mediated by DWF4, CPD (Szerkeres et al. (1996), *supra*), DET2 (Fujioka and Skaurai (1997a), *infra*; Li et al. (1997), *supra*) and LKB (Yokota et al. (1997), *infra*) are indicated.

Please replace the paragraph beginning at page 11, line 31 as with the following amended paragraph:

~~Figure 3~~Figures 3A and 3B ~~depicts~~ depict an alignment of cytochrome P450 proteins that exhibited the most similarity to DWF4 (SEQ. ID NO:2) in BLAST searches. GenBank accession numbers are AF044216 (DWF4; CYP90B) (SEQ. ID NO:2), X87368 (CPD; CYP90A), U54770 (tomato; CYP85), D64003 (cyanobacteria; CYP120), U32579 (maize; CYP88), U68234 (zebrafish; CYP26), and M13785 (human; CYP3A3X). Dashes indicate gaps introduced to maximize alignment. Domains indicated in Figure 2B are highlighted in a box. Amino acid residues that are conserved >50% between the compared sequences are highlighted by a reverse font, and identical residues between DWF4 and CPD are boxed and italicized. Open triangles are placed under the 100% conserved residues. Closed triangles locate functionally important amino acid residues, for example, threonine (T) at 369, which is thought to bind molecular oxygen, and cysteine (C) at 516, which links to a heme prosthetic group by a thiolate bond. X's indicate mutated residues in *dwf4* alleles. Multiple sequence alignment was performed using PILEUP in the Genetics Computer Group package, and box shading was made possible by the ALSCRIPT package (Barton (1993) *Protein Eng.* 6:37-40).

Please replace the paragraph beginning at page 13, line 24 as with the following amended paragraph:

Figures 10(A)-10~~(G)~~(M) depict the nucleotide sequence of wild-type *dwf4* (SEQ ID NO:1, *see, also*, GenBank Accession Number AF044216). The *dwf4* polynucleotide includes a coding region between nucleotides 3203 and 6110, inclusive. The coding region includes the following eight exons: nucleotides 3203 to 3423, inclusive; nucleotides 3504 to 3828, inclusive; nucleotides 3914 to 4066, inclusive; nucleotides 4165 to 4479, inclusive; nucleotides 4632 to 4724, inclusive; nucleotides 4816 to 4894, inclusive; nucleotides 5001 to 5110, inclusive and nucleotides 5865 to 6110, inclusive. The exons are indicated by a bar beneath the nucleotide sequence. A 5' control region (e.g., promoter) extends from nucleotides 1 to 3202. A 3' untranslated region (UTR), corresponds to the region extending from nucleotide to 6011 to approximately nucleotide 6468 of Figure 10 (SEQ ID NO:1) and a TATA signal extending approximately from nucleotides 3060 to 3125. As described in the Examples, mutant alleles of *dwf4* have also been characterized. For example, *dwf4-1* contains an approximately 20 kb insert between nucleotides 5202 and 5203. *dwf4-2* has a 9 base pair deletion corresponding to amino acids 324-326. In mutant allele *dwf4-3*, the guanine (G) residue at position 4332 is replaced with an adenine (A) residue to create a premature stop codon and truncate the DWF4 protein at amino acid 289.

Please replace the paragraph beginning at page 30, line 22 as with the following amended paragraph:

Regulatory regions can be isolated from the dwf4 gene and used in recombinant constructs for modulating the expression of the dwf4 gene or a heterlogous gene in vitro and/or in vivo. As shown in Figure 10, the coding region of the dwf4 gene (designated by the ~~light grey bar~~ open bar) begins at nucleotide position 1133. The region of the gene spanning nucleotide positions 990-1132 of Figure 10 includes the *dwf4* promoter. This region may be used in its entirety or fragments of the region may be isolated which provide the ability to direct expression of a coding sequence linked thereto.